SEQUENCE LISTING

<110> Sedivy, John
Kolch, Walter
Yeung, Kam Chi

<120> Kinase Inhibitors and Methods of Use in Screening Assays and Modulation of Cell Proliferation and Growth

<130> 3564/1010

<140> 09/654,281
<141> 2000-09-01

<150> 60/151,992
<151> 1999-09-01

<160> 11

<170> PatentIn version 3.0

<210> 1
<211> 42
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

<220>
<221> UNSURE
<222> (3)..(5)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (9)..(9)
<223> a hydrophobic amino acid residue

<220>
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<222> (11)..(13)
<223> Xaa = any amino acid

<220>
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<222> (14)..(14)
<223> a negatively charged amino acid residue

<220>
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<222> (15)..(18)
<223> Xaa = any amino acid residue

<220>
<221> UNSURE
<222> (20)..(21)
<223> Xaa = any amino acid residue

<220>
<221> UNSURE
<222> (23)..(23)
<223> Xaa = 50 of any amino acid residue, 0 to 40 residues may be miss
ing

cont.

<220>
<221> UNSURE
<222> (25)..(28)
<223> Xaa = any amino acid residue

<220>
<221> UNSURE
<222> (30)..(30)
<223> Xaa = 4 of any amino acid residue, 0 to 2 residues may be missin
g

<220>
<221> UNSURE
<222> (32)..(32)
<223> Xaa = any amino acid residue

<220>
<221> UNSURE
<222> (35)..(35)
<223> Xaa = an aromatic amino acid residue

<220>
<221> UNSURE
<222> (37)..(37)
<223> Xaa = any amino acid residue

<220>
<221> UNSURE
<222> (38)..(38)
<223> a hydrophobic amino acid residue

<220>
<221> UNSURE
<222> (39)..(41)
<223> Xaa = any amino acid residue

<400> 1

Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
1 5 10 15

Xaa Xaa Glu Xaa Xaa His Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Gly Xaa
20 25 30

His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
35 40

C1 cont

<210> 2
<211> 187
<212> PRT
<213> Homo sapiens

<400> 2

Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
1 5 10 15

Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
20 25 30

Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
35 40 45

Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
50 55 60

Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
65 70 75 80

Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
85 90 95

Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
100 105 110

Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp

```
        115                 120                 125

Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
    130                 135                 140

His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
145                 150                 155                 160

Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
                165                 170                 175

Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
            180                 185
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<210> 3
<211> 187
<212> PRT
<213> Mus musculus

<220>
<221> UNSURE
<222> (150)..(150)
<223> Xaa = any amino acid residue

<400> 3

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Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
1               5                   10                  15

Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
            20                  25                  30

Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
        35                  40                  45

Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
    50                  55                  60

Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
65                  70                  75                  80

Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
                85                  90                  95

Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
            100                 105                 110

Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
        115                 120                 125

Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
```

130 135 140

Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
145 150 155 160

Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
165 170 175

Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
180 185

<210> 4
<211> 187
<212> PRT
<213> Drosophila

<400> 4

Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
1 5 10 15

Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
20 25 30

Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
35 40 45

Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
50 55 60

Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
65 70 75 80

Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
85 90 95

Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
100 105 110

Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
115 120 125

Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
130 135 140

Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
145 150 155 160

Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
165 170 175

Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys

C1 cont

180 185

<210> 5
<211> 220
<212> PRT
<213> C. elegans

<400> 5

Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
1 5 10 15

Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
20 25 30

Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
35 40 45

Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
50 55 60

Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
65 70 75 80

Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
85 90 95

Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
100 105 110

Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
115 120 125

Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
130 135 140

Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
145 150 155 160

Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
165 170 175

Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
180 185 190

Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
195 200 205

Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
210 215 220

<210> 6

C1 cont.

<211> 181
<212> PRT
<213> Antirrhinum-CEN

<400> 6

Met Ala Ala Lys Val Ser Ser Asp Pro Leu Val Ile Gly Arg Val Ile
1 5 10 15

Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
20 25 30

Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
35 40 45

Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
50 55 60

Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
65 70 75 80

Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
85 90 95

Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
100 105 110

Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
115 120 125

Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
130 135 140

Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
145 150 155 160

Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
165 170 175

Ala Ala Arg Arg Arg
180

<210> 7
<211> 176
<212> PRT
<213> Aradopsis-TFL1

<400> 7

Met Glu Asn Met Gly Thr Arg Val Ile Glu Pro Leu Ile Met Gly Arg
1 5 10 15

C/cont.

Val Val Gly Asp Val Leu Asp Phe Phe Thr Pro Thr Thr Lys Met Asn
20 25 30

Val Ser Tyr Asn Lys Lys Gln Val Asn Gly His Glu Leu Phe Pro Ser
35 40 45

Ser Val Ser Ser Lys Pro Arg Val Glu Ile His Gly Gly Asp Leu Arg
50 55 60

Ser Phe Phe Thr Leu Val Met Ile Asp Pro Asp Val Pro Gly Pro Ser
65 70 75 80

Asp Pro Phe Leu Lys Glu His Leu His Trp Ile Val Thr Asn Ile Pro
85 90 95

Gly Thr Thr Asp Ala Thr Phe Gly Lys Glu Val Val Ser Tyr Glu Leu
100 105 110

Pro Arg Pro Ser Ile Gly Ile His Arg Phe Val Phe Val Leu Phe Arg
115 120 125

Gln Lys Gln Arg Arg Val Ile Phe Pro Asn Ile Pro Ser Arg Asp His
130 135 140

Phe Asn Thr Arg Lys Phe Ala Val Glu Tyr Asp Leu Gly Leu Pro Val
145 150 155 160

Ala Ala Val Phe Phe Asn Ala Gln Arg Glu Thr Ala Ala Arg Lys Arg
165 170 175

<210> 8
<211> 219
<212> PRT
<213> Yeast

<400> 8

Met Asn Gln Ala Ile Asp Phe Ala Gln Ala Ser Ile Asp Ser Tyr Lys
1 5 10 15

Lys His Gly Ile Leu Glu Asp Val Ile His Asp Thr Ser Phe Gln Pro
20 25 30

Ser Gly Ile Leu Ala Val Glu Tyr Ser Ser Ser Ala Pro Val Ala Met
35 40 45

Gly Asn Thr Leu Pro Thr Glu Lys Ala Arg Ser Lys Pro Gln Phe Gln
50 55 60

Phe Thr Phe Asn Lys Gln Met Gln Lys Ser Val Pro Gln Ala Asn Ala
65 70 75 80

C /cont.

Tyr Val Pro Gln Asp Asp Asp Leu Phe Thr Leu Val Met Thr Asp Pro
85 90 95

Asp Ala Pro Ser Lys Thr Asp His Lys Trp Ser Glu Phe Cys His Leu
100 105 110

Val Glu Cys Asp Leu Lys Leu Leu Asn Glu Ala Thr His Glu Thr Ser
115 120 125

Gly Ala Thr Glu Phe Phe Ala Ser Glu Phe Asn Thr Lys Gly Ser Asn
130 135 140

Thr Leu Ile Glu Tyr Met Gly Pro Ala Pro Pro Lys Gly Ser Gly Pro
145 150 155 160

His Arg Tyr Val Phe Leu Leu Tyr Lys Gln Pro Lys Gly Val Asp Ser
165 170 175

Ser Lys Phe Ser Lys Ile Lys Asp Arg Pro Asn Trp Gly Tyr Gly Thr
180 185 190

Pro Ala Thr Gly Val Gly Lys Trp Ala Lys Glu Asn Asn Leu Gln Leu
195 200 205

Val Ala Ser Asn Phe Phe Tyr Ala Glu Thr Lys
210 215

C/cont.

<210> 9
<211> 189
<212> DNA
<213> Homo sapiens

<400> 9
accttggtcc tgacagaccc ggatgctccc agcaggaagg atcccaaata cagagaatgg 60

catcatttcc tggtggtcaa catgaagggc aatgacatca gcagtggcac agtcctctcc 120

gattatgtgg gctcggggcc tcccaagggc acaggcctgc accgctatgt ctggctggtt 180

tacgagcag 189

<210> 10
<211> 7
<212> DNA
<213> Artificial/Unknown

<220>

<221> Unsure
<222> (4)..(4)
<223> n = C or G

<220>
<221> misc_feature
<223> Consensus AP-1 binding site

<400> 10
tgantca
7

C / CONTD

<210> 11
<211> 11
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<223> NF-kB binding element consensus sequence

<400> 11
ggggactttc c 1
1